FIG.1

```
1     ATGCTAACCTTCCCGTTGAGCCCGAGTTCGAGCAGGCCTACAAGGAGCTTGCGTCGACC
      ***********************************************************
2     ATGCTAACCTTCCCGTTGAGCCCGAGTTCGAGCAGGCCTACAAGGAGCTTGCGTCGACC

61    CTCGAGAACTCCACCCTCTTTGAGCAGCACCCTGAATACCGACGGGCTCTCCAGGTCGTC
      ***********************************************************
61    CTCGAGAACTCCACCCTCTTTGAGCAGCACCCTGAATACCGACGGGCTCTCCAGGTCGTC

121   TCCGTTCCCGAGCGCGTTATCCAGTTCCGTGTCGTTTGGGAGAACGACAAGGGCGAGGTT
      ***********************************************************
121   TCCGTTCCCGAGCGCGTTATCCAGTTCCGTGTCGTTTGGGAGAACGACAAGGGCGAGGTT

181   CAGATCAACCGCGGTTACCGTGTTCAGTTCAACTCCGCTCTCGGTCCCTACAAGGGTGGT
      ***********************************************************
181   CAGATCAACCGCGGTTACCGTGTTCAGTTCAACTCCGCTCTCGGTCCCTACAAGGGTGGT

241   CTCCGTTTCCACCCCTCCGTCAACCTTTCTATCCTGAAGTTCCTTGGCTTCGAGCAGATC
      ***********************************************************
241   CTCCGTTTCCACCCCTCCGTCAACCTTTCTATCCTGAAGTTCCTTGGCTTCGAGCAGATC

301   TTCAAAAATGCTCTCACAGGAC[ ◄——————————  Splicing site
      *********************
301   TTCAAAAATGCTCTCACAGGACGTGCGTAACCGTTACTTCATTGGATGTTTGCCAAGAGT

323        ——————————►]TAAACATGGGTGGTGGCAAGGGTGGTTCCGACTTCGACCCCAAGG
                       ****************************************
361   ACTAATTGGTATTAGTAAACATGGGTGGTGGCAAGGGTGGTTCCGACTTCGACCCCAAGG

368   GCAAGTCTGACTCTGAAATTCGTCGCTTCTGTACCGCTTTCATGACTGAGCTCTGCAAGC
      ***********************************************************
421   GCAAGTCTGACTCTGAAATTCGTCGCTTCTGTACCGCTTTCATGACTGAGCTCTGCAAGC

428   ACATCGGCGCGGACACTGACCTTCCCGCTGGTGATATCGGTGTTACTGGCCGTGAGGTTG
      ***********************************************************
481   ACATCGGCGCGGACACTGACCTTCCCGCTGGTGATATCGGTGTTACTGGCCGTGAGGTTG

488   GTTTCCTTTTCGGCCAGTACCGCAGGATCCGCAACCAGTGGGAGGGTGTTCTCACTGGCA
      ***********************************************************
541   GTTTCCTTTTCGGCCAGTACCGCAGGATCCGCAACCAGTGGGAGGGTGTTCTCACTGGCA

548   AGGGTGGCAGCTGGGGTGGTAGCTTGATCCGCCCTGAAGCCACTGGATACGGTGTTGTCT
      ***********************************************************
601   AGGGTGGCAGCTGGGGTGGTAGCTTGATCCGCCCTGAAGCCACTGGATACGGTGTTGTCT

608   ACTACGTTCAGCACATGATCAAGCACGTTACCGGTGGAAAGGAGTCCTTCGCAGGCAAGC
      ***********************************************************
661   ACTACGTTCAGCACATGATCAAGCACGTTACCGGTGGAAAGGAGTCCTTCGCAGGCAAGC
```

FIG.2

668	GTGTCGCCATCTCCGGCTCCGGTAACGTTGCCCAGTACGCCGCTCTCAAGGTCATCGAGC
	**
721	GTGTCGCCATCTCCGGCTCCGGTAACGTTGCCCAGTACGCCGCTCTCAAGGTCATCGAGC
728	TCGGTGGTTCCGTTGTCTCCCTTTCCGACTCCAAGGGCTCTCTCATTGTCAAGGATGAGT
	**
781	TCGGTGGTTCCGTTGTCTCCCTTTCCGACTCCAAGGGCTCTCTCATTGTCAAGGATGAGT
788	CCGCTTCTTTCACCCCTGAAGAGATCGCCCTCATTGCCGACCTCAAGGTTGCCCGCAAGC
	**
841	CCGCTTCTTTCACCCCTGAAGAGATCGCCCTCATTGCCGACCTCAAGGTTGCCCGCAAGC
848	AACTCTCCGAGCTCGCCACCTCCTCCGCTTTCGCCGGCAAGTTCACCTACATCCCCGATG
	**
901	AACTCTCCGAGCTCGCCACCTCCTCCGCTTTCGCCGGCAAGTTCACCTACATCCCCGATG
908	CTCGCCCTTGGACCAACATTCCCGGCAAGTTCGAGGTTGCTCTCCCTTCTGCCACTCAGA
	**
961	CTCGCCCTTGGACCAACATTCCCGGCAAGTTCGAGGTTGCTCTCCCTTCTGCCACTCAGA
968	ACGAAGTCTCCGGCGAGGAAGCCGAGCACCTCATCAAGTCCGGTGTCCGCTATATTGCTG
	**
1021	ACGAAGTCTCCGGCGAGGAAGCCGAGCACCTCATCAAGTCCGGTGTCCGCTATATTGCTG
1028	AGGGTTCCAACATGGGTTGCACCCAGGCCGCCATCGACATCTTTGAGGCTCACCGCAACG
	**
1081	AGGGTTCCAACATGGGTTGCACCCAGGCCGCCATCGACATCTTTGAGGCTCACCGCAACG
1088	CCAACCCCGGCGATGCCATCTGGTACGCCCCTGGTAAAGCCGCCAACGCTGGTGGTGTCG
	**
1141	CCAACCCCGGCGATGCCATCTGGTACGCCCCTGGTAAAGCCGCCAACGCTGGTGGTGTCG
1148	CCGTCTCTGGTCTTGAGATGGCTCAGAACTCTGCTCGTCTCTCCTGGACATCCGAGGAGG
	**
1201	CCGTCTCTGGTCTTGAGATGGCTCAGAACTCTGCTCGTCTCTCCTGGACATCCGAGGAGG
1208	TCGATGCTCGCCTCAAGGGCATCATGGAGGACTGCTTCAAGAACGGTCTCGAGACTGCTC
	**
1261	TCGATGCTCGCCTCAAGGGCATCATGGAGGACTGCTTCAAGAACGGTCTCGAGACTGCTC
1268	AGAAGTTCGCTACTCCTGCCAAGGGCGTCCTGCCTTCCCTCGTCACCGGTTCCAACATTG
	**
1321	AGAAGTTCGCTACTCCTGCCAAGGGCGTCCTGCCTTCCCTCGTCACCGGTTCCAACATTG
1328	CCGGTTTCACCAAGGTCGCCGAGGCCATGAAGGACCAGGGTGACTGGTGGTGA
	**
1381	CCGGTTTCACCAAGGTCGCCGAGGCCATGAAGGACCAGGGTGACTGGTGGTGA

FIG.3

FIG.4

Ti-plasmid: pMAT037
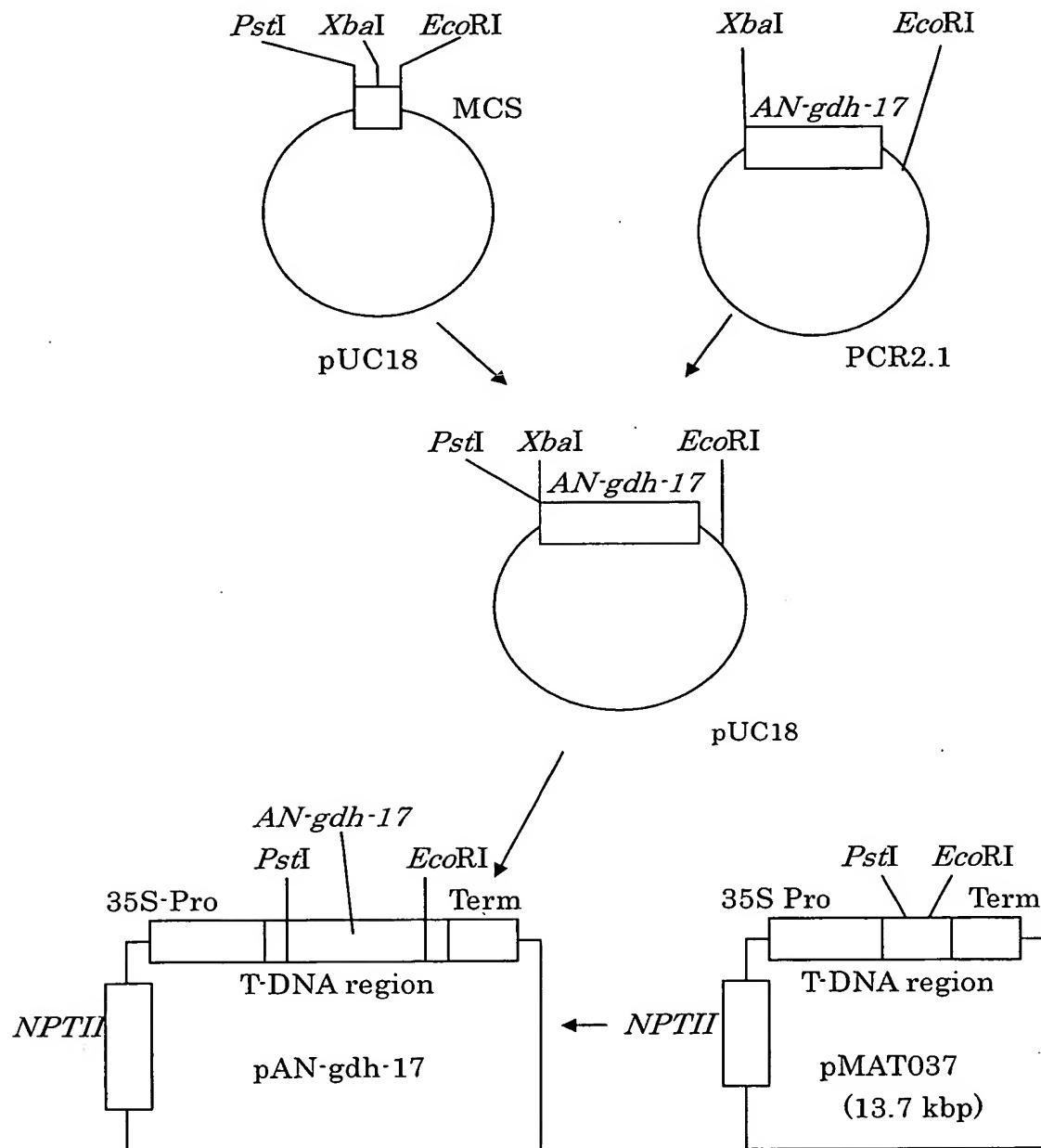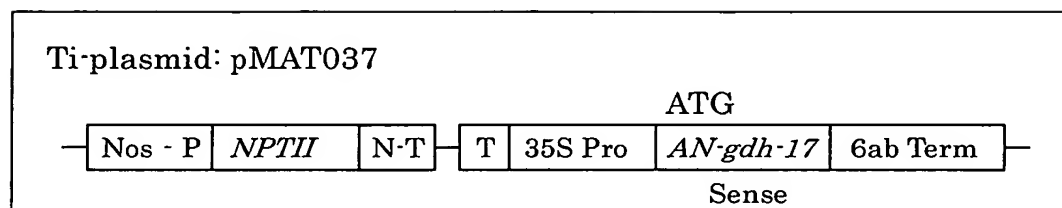
| | Nos - P | *NPTII* | N-T | | T | 35S Pro | *AN-gdh-17* | 6ab Term | |

ATG

Sense

Ti - plasmid: pIG121-Hm (35S promoter is used)

| | Nos-P | *NPTII* | N-T | | 35S Pro | *AN-gdh-17* | N-T | | 35S-Pro | *HPT* | N-T | |

Sense

(1)   pCt-AN-gdh

| Ct-trans | | | *AN-gdh-17* (containing splicing region) |

Added the coding sequence for chloroplast transit peptide (rbcS)

(2) pCt-dAN-gdh
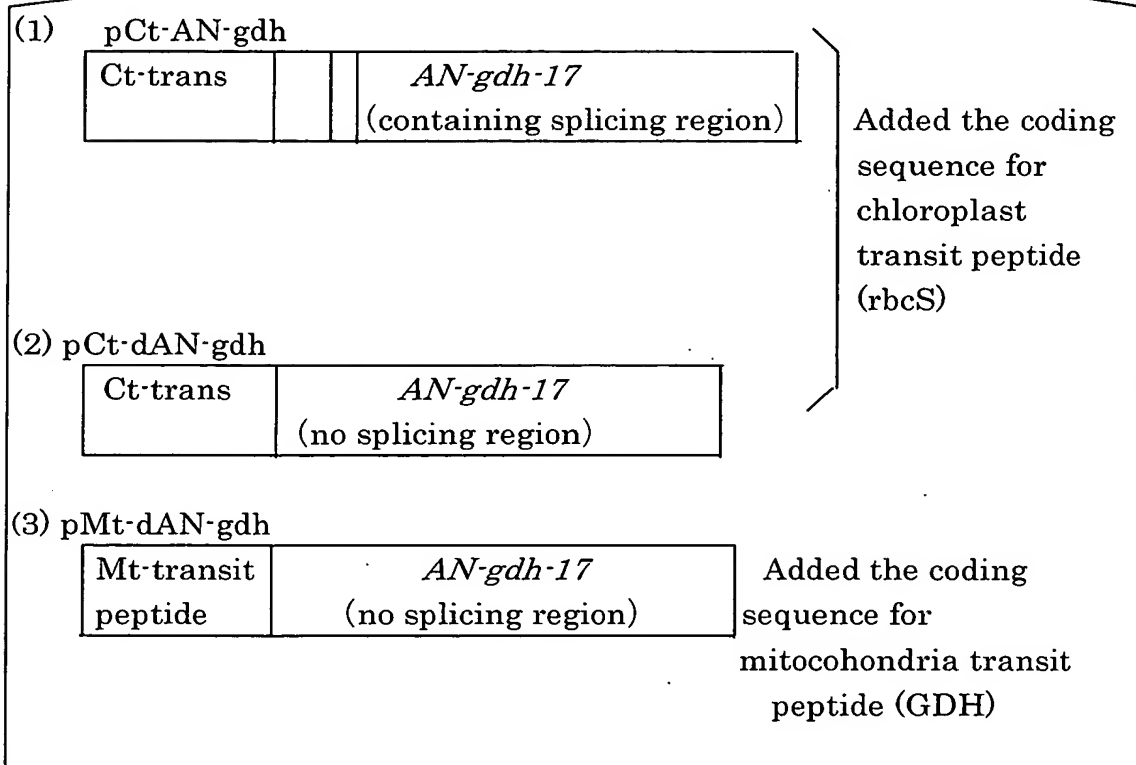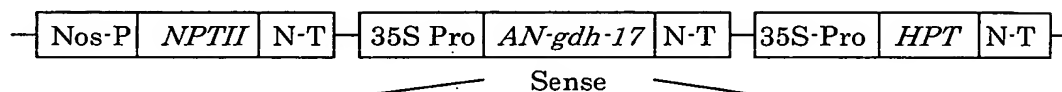
| Ct-trans | *AN-gdh-17* (no splicing region) |
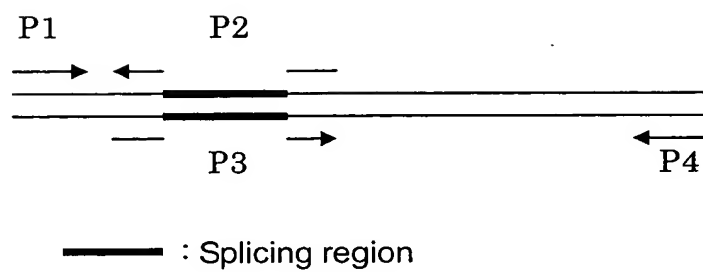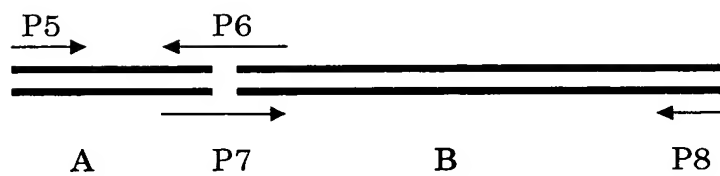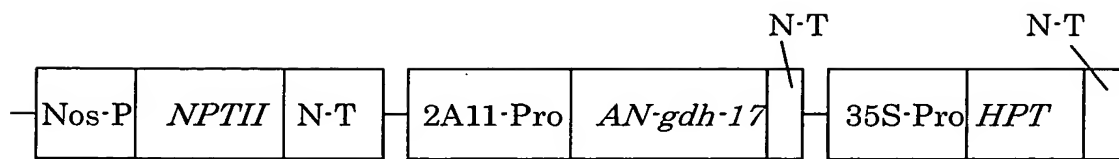
(3) pMt-dAN-gdh

| Mt-transit peptide | *AN-gdh-17* (no splicing region) |

Added the coding sequence for mitocohondria transit peptide (GDH)

FIG.5

P1   P2

P3

P4

■■■■■ : Splicing region

FIG.6

P5   P6

A   P7   B   P8

FIG.7

FIG.8

FIG.9

Ti-plasmid: pT-gdh-4

| —| Nos-P | NPTII | N-T | | 35S-Pro | *T-gdh-4* | Nos | | 35S-P | *HPT* | N-T | — |

Sense

↓

Substitution of amino acids in the glutamine binding site
(Lys-90, Thr-169, Ser-345)

↓

| Lys-90 | ——————→ | Ala-90 |
| (AAG) | | (GCG) |

↓

Ti-plasmid: pTd-gdh

| —| Nos-P | *NPTII* | N-T | | 35S-Pro | *Td-gdh* | Nos | | 35S-P | *HPT* | N-T | — |

Sense
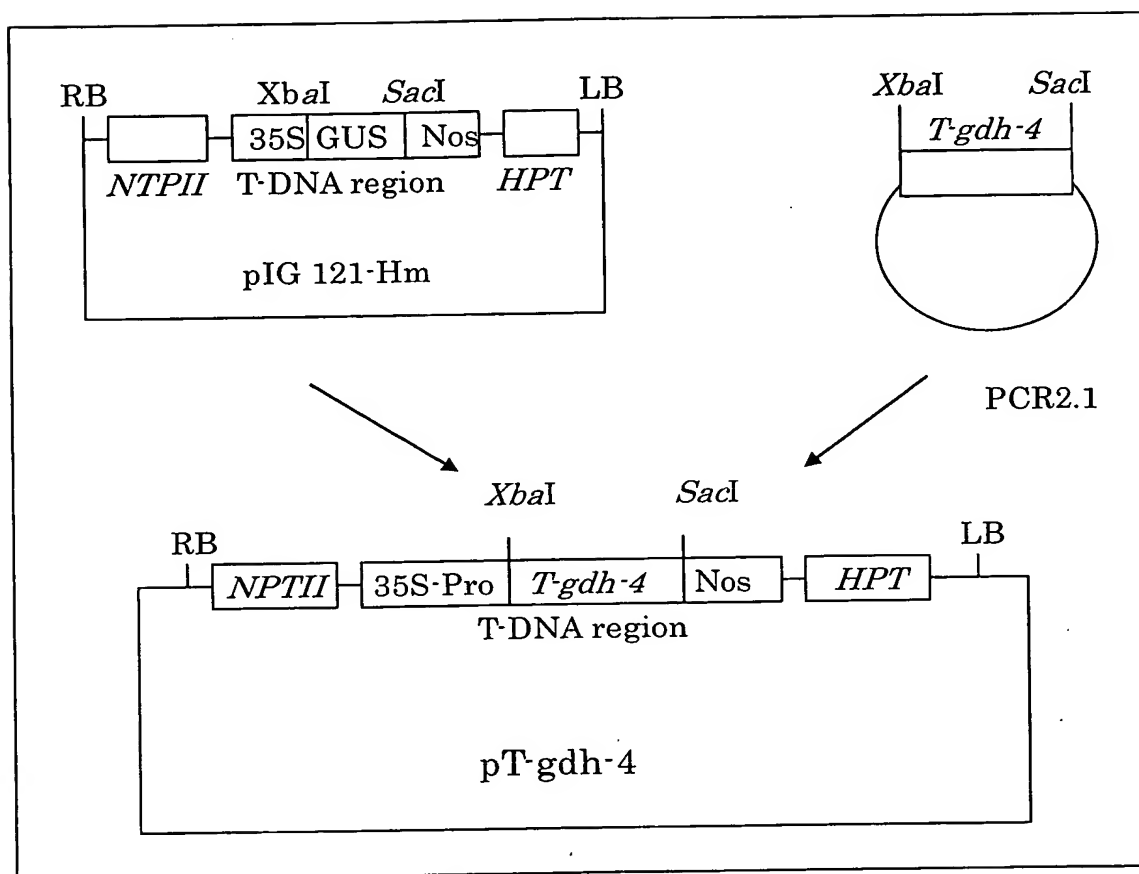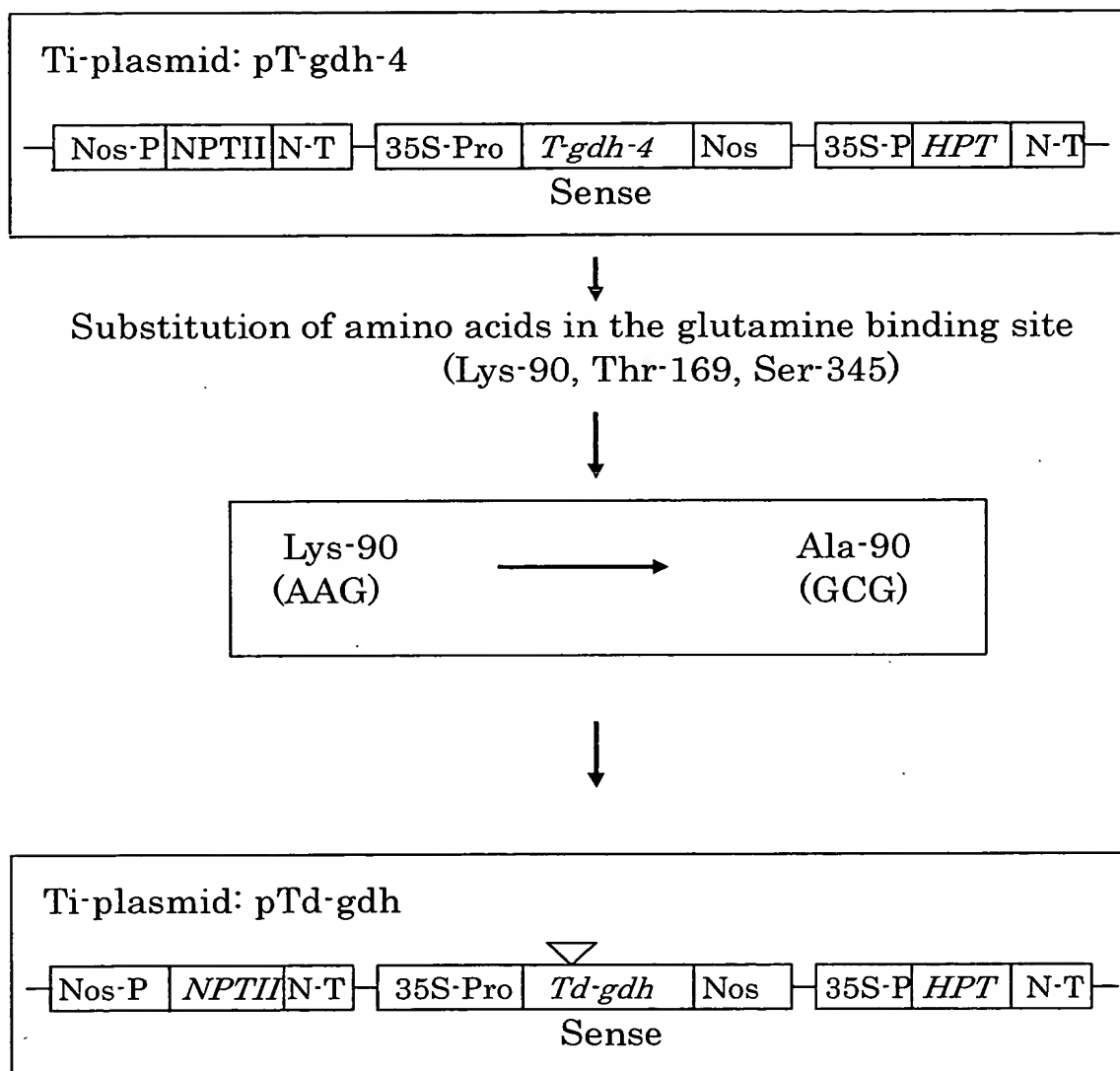
FIG.10
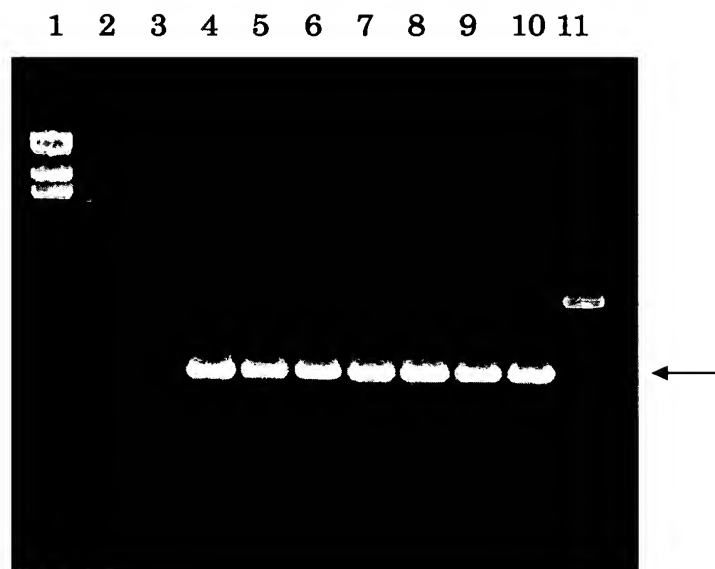
1. γ-*Hin*dIII marker
2. Untransformed tomato no. 1
3. Untransformed tomato no. 2
4. pMAT037 no. 1
5. pMAT037 no. 2
6. pMAT037 no. 3
7. AN-gdh-17 no. 6
8. AN-gdh-17 no. 8-2
9. AN-gdh-17 no. 15
10. AN-gdh-17 no. 17
11. 100bp marker

FIG.11

1. γ-*Hind*III marker
2. Untransformed tomato no. 1
3. Untransformed tomato no. 2
4. pIG121 no. 1
5. pIG121 no. 2
6. pIG121 no. 3
7. T-gdh-4 no. 2
8. T-gdh-4 no. 7-2
9. T-gdh-4 no. 9-2
10. T-gdh-4 no. 10
11. 100bp marker
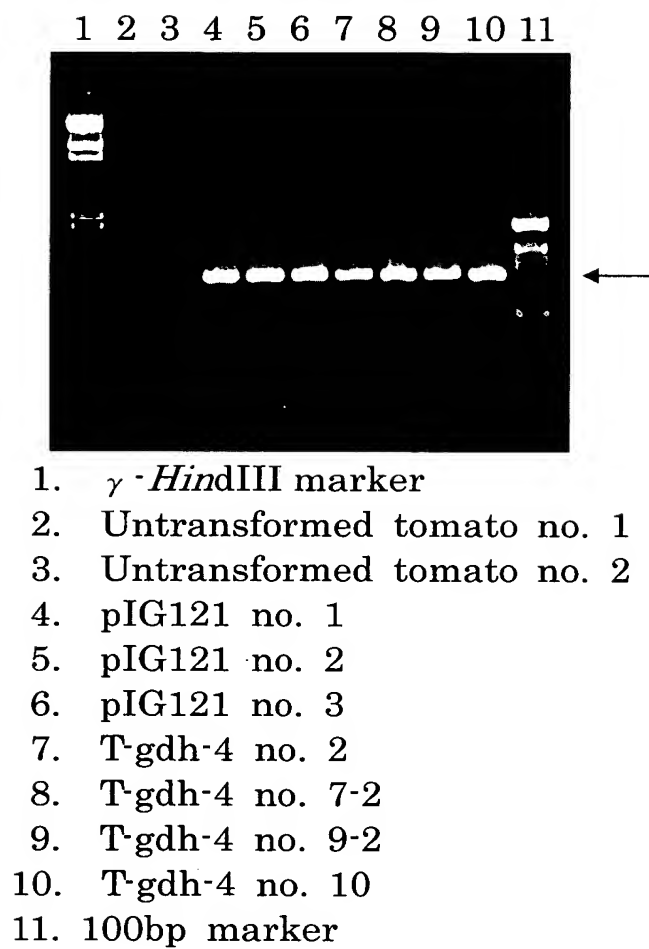
FIG.12
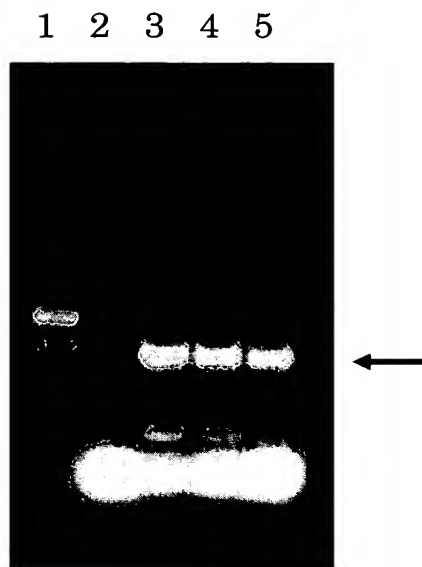
1. 100 bp marker
2. Untransformed tomato (leaf)
3. AN-gdh-17 no. 6 (leaf)
4. AN-gdh-17 no. 15 (leaf)
5. AN-gdh-17 no. 6 (fruit)

FIG.13
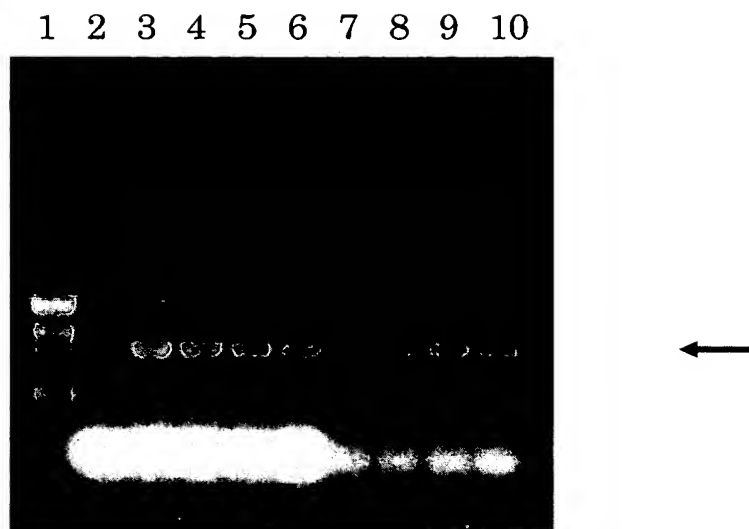
1. 100 bp marker   2. Untransformed-tomato (leaf)
3. T-gdh-4 no. 2 (leaf)   4. T-gdh-4 no. 7-2 (leaf)
5. T-dgh-4 no. 9-2 (leaf)   6. T-gdh-4 no. 10 (leaf)
7. T-gdh-4 no. 2 (fruit)   8. T-gdh-4 no. 7-2 (fruit)
9. T-gdh-4 no. 9-2 (fruit)   10. T-gdh-4 no. 10 (fruit)

FIG.14
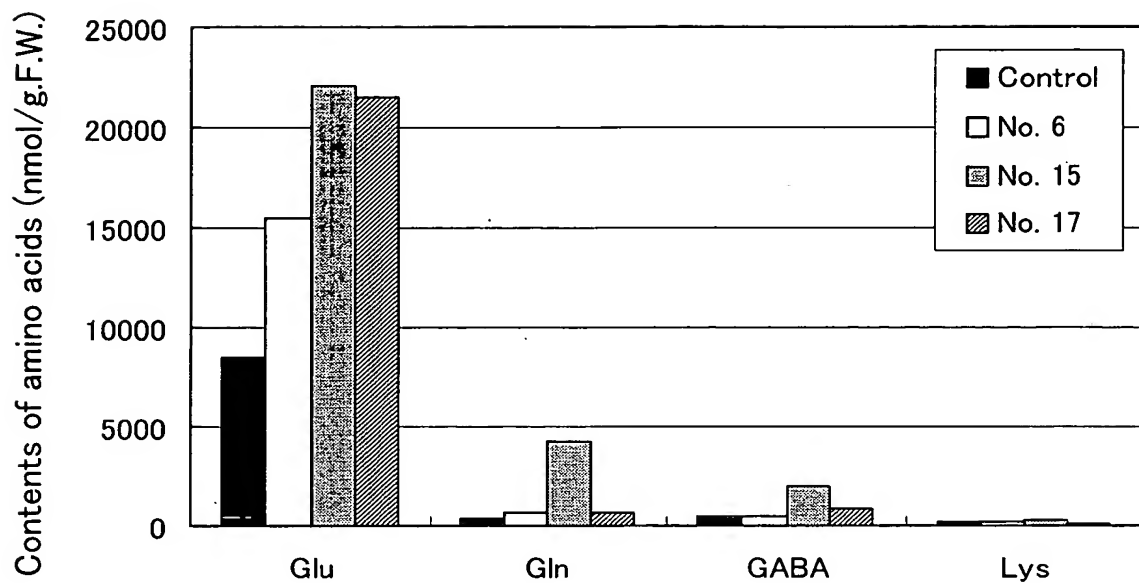
FIG.15
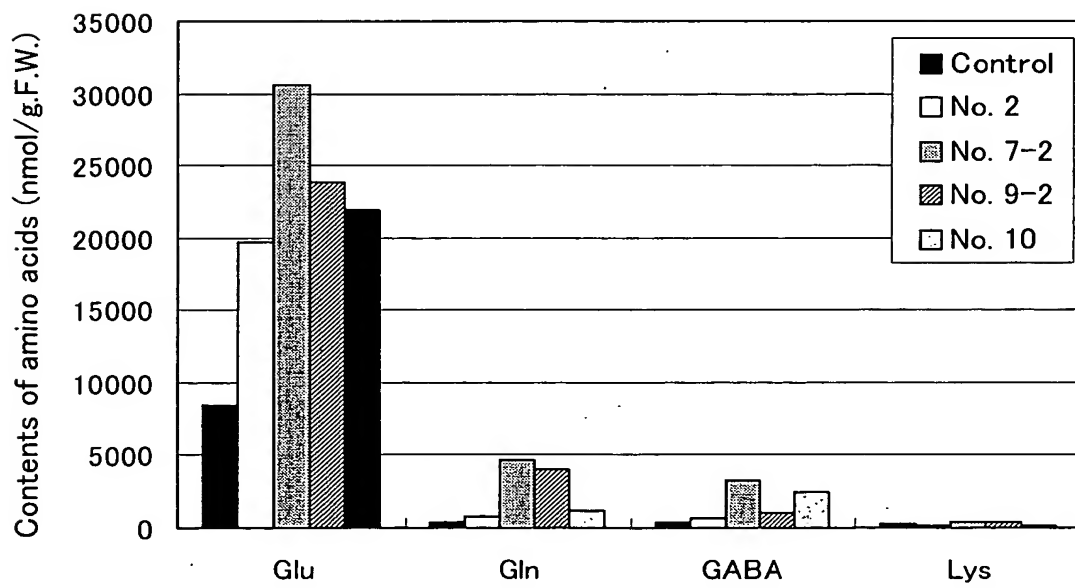
FIG.16
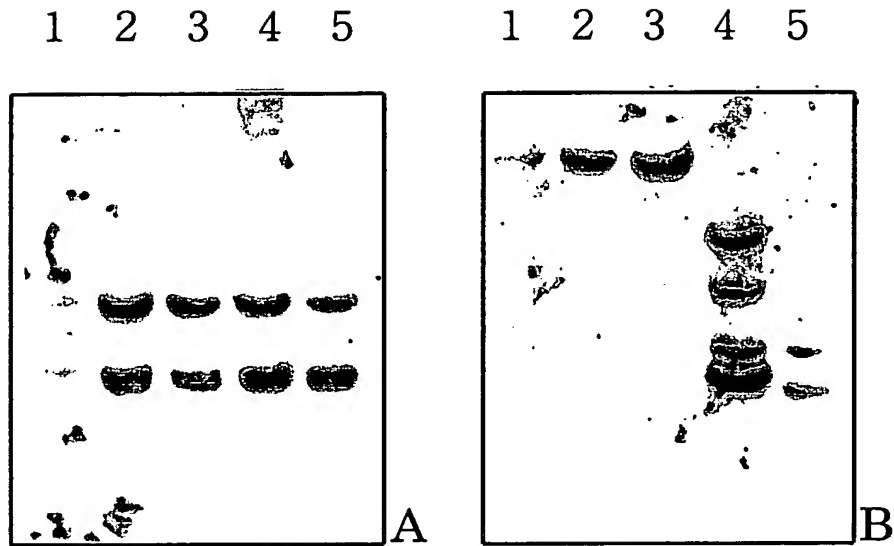
Lanes
1. Non-transgenic tomato
2. AN-gdh-17 No.1
3. AN-gdh-17 No.3
4. AN-gdh-17 No.15
5. AN-gdh-17 No.2.1

A. Total DNA(15 μ g) was digested with *Bam*HI and *Eco*RI.

B. Total DNA(15 μ g) was digested with *Xba*I.

FIG. 17

1 2 3 4
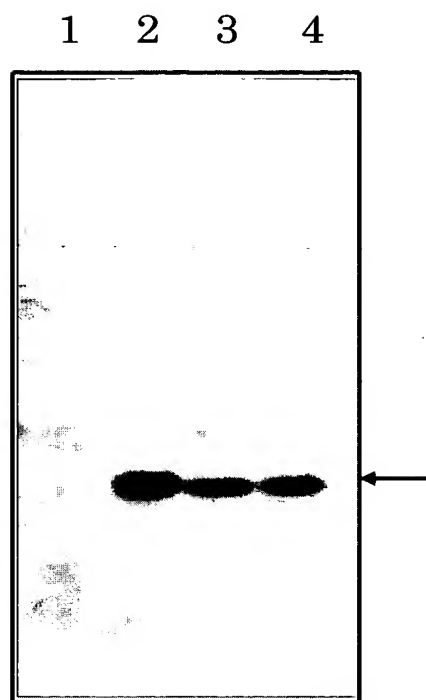
FIG.18

Amino acid contents in fruits of the progenies (T₁) of
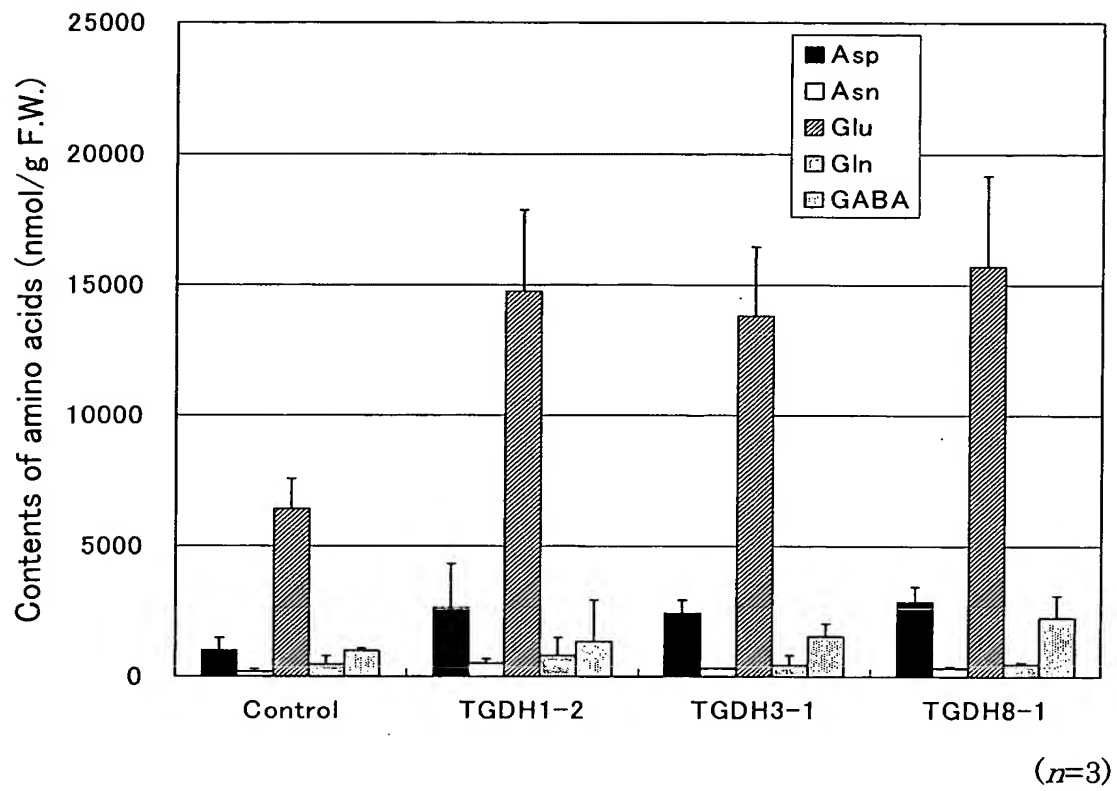
AN-gdh-17 gene introduced tomato transformants

(n=3)

FIG.19

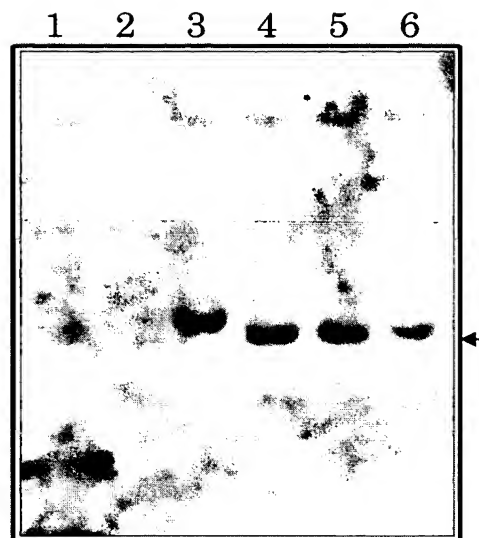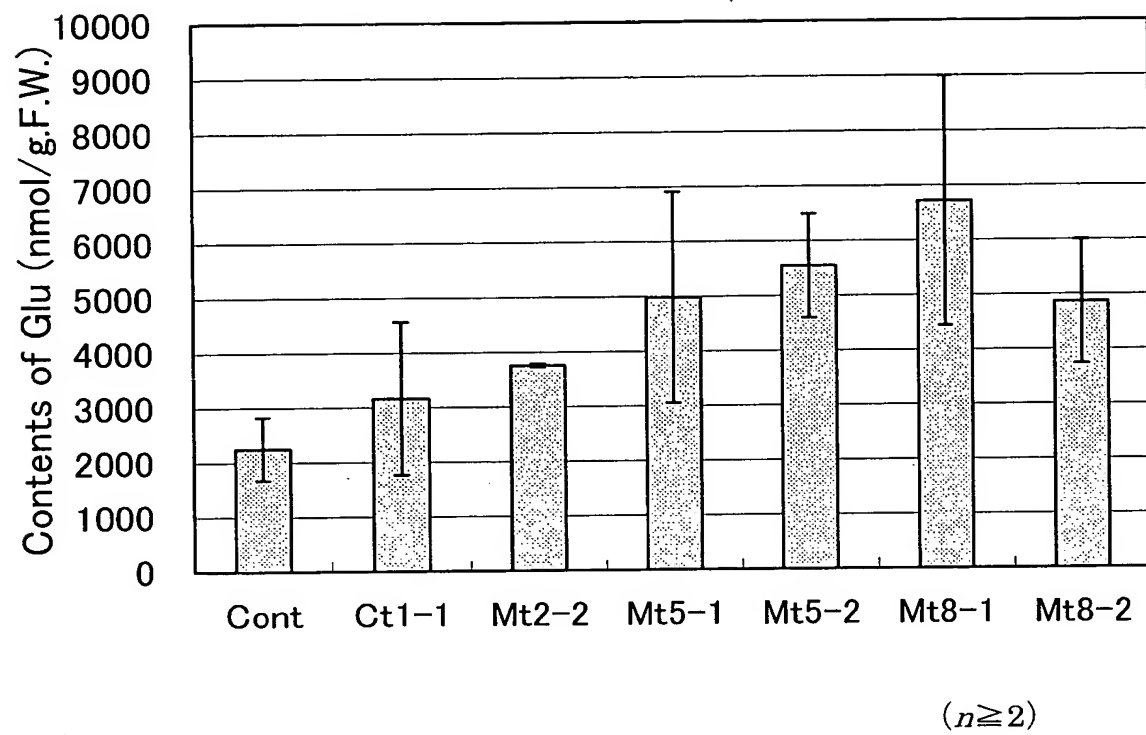(n=3)

FIG.20

FIG.21

(*n*≧2)

FIG.22

FIG.23